

Genome version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

EM nucleic nucleic search, using sw model

Run on: April 16, 2003, 22:48:44 : Search time 658 Seconds

(without alignments)

10021.050 Million cell updates/sec

Title: US-09-954-679-3

Perfect score: 2928

Sequence: 1 autccacattacactcadd.....qqqqccttqqatqqatqqat: 2928

Scoring table: IDENTITY_NOR

Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2274872

Minimum DB seq length: 0

Maximum DB seq length: 60

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA1980.DAT: *
2: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA1981.DAT: *
3: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA1982.DAT: *
4: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA1983.DAT: *
5: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA1984.DAT: *
6: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA1985.DAT: *
7: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA1986.DAT: *
8: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA1987.DAT: *
9: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA1988.DAT: *
10: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA1989.DAT: *
11: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA1990.DAT: *
12: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA1991.DAT: *
13: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA1992.DAT: *
14: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA1993.DAT: *
15: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA1994.DAT: *
16: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA1995.DAT: *
17: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA1996.DAT: *
18: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA1997.DAT: *
19: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA1998.DAT: *
20: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA1999.DAT: *
21: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA2000.DAT: *
22: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA2001A.DAT: *
23: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA2001B.DAT: *
24: /SUS2/qqqdat/a/geneseq/geneseq-emb1/NA2002.DAT: *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 45 | 1.2 | 35 | AA146192 | Primer for ribonuc |
| 2 | 45 | 1.2 | 45 | AA146191 | Primer for ribonuc |
| 3 | 25.6 | 0.9 | 60 | ABN47026 | Human spliced tran |
| 4 | 25 | 0.9 | 48 | AAV46756 | Nucleotide sequenc |
| 5 | 25 | 0.9 | 48 | AAV40768 | RNase L PCR primer |
| 6 | 24.8 | 0.8 | 47 | AA266719 | Human map-related |
| 7 | 24.6 | 0.8 | 51 | AA128761 | Human Snp oligonuc |
| 8 | 24.6 | 0.8 | 60 | ABN45766 | Human spliced tran |
| 9 | 24.4 | 0.8 | 60 | ABN47378 | Human spliced tran |

| | | | | | | |
|------|------|-----|----|----|----------|-----------------------|
| C 10 | 23.4 | 0.8 | 60 | 24 | ABN40943 | Human spliced tran |
| C 11 | 23.2 | 0.8 | 60 | 24 | ABN48713 | Human spliced tran |
| C 12 | 22.8 | 0.8 | 60 | 24 | ABN46051 | Human spliced tran |
| C 13 | 22.8 | 0.8 | 60 | 24 | ABN42702 | Primer for human co |
| C 14 | 22.6 | 0.8 | 40 | 17 | AA128117 | Human spliced tran |
| C 15 | 22.6 | 0.8 | 60 | 24 | ABN45589 | Human spliced tran |
| C 16 | 22.6 | 0.8 | 60 | 24 | ABN40697 | Human spliced tran |
| C 17 | 22.4 | 0.8 | 57 | 16 | AA122865 | Human cdc28 cDNA |
| C 18 | 22.4 | 0.8 | 58 | 24 | AA155233 | 5' cDNA encoding pro |
| C 19 | 22.4 | 0.8 | 59 | 21 | AA196905 | Human Snp oligonuc |
| C 20 | 22.2 | 0.8 | 51 | 22 | AA128440 | cDNA encoding more |
| C 21 | 22.2 | 0.8 | 51 | 22 | AA159488 | Human Snp oligonuc |
| C 22 | 22.2 | 0.8 | 51 | 22 | AA198855 | Yeast tetracycline |
| C 23 | 22.2 | 0.8 | 60 | 21 | AA157910 | Human Snp oligonuc |
| C 24 | 22.2 | 0.8 | 60 | 24 | ABN43058 | Human spliced tran |
| C 25 | 22 | 0.8 | 51 | 22 | AA155030 | Human Snp oligonuc |
| C 26 | 22 | 0.8 | 58 | 19 | AAV28959 | Human Snp oligonuc |
| C 27 | 22 | 0.8 | 60 | 24 | ABN48594 | Human spliced tran |
| C 28 | 22 | 0.8 | 60 | 24 | ABN40101 | Human spliced tran |
| C 29 | 22 | 0.8 | 60 | 24 | ABN40981 | Human spliced tran |
| C 30 | 21.8 | 0.7 | 39 | 19 | AAV13828 | Primer for canine |
| C 31 | 21.8 | 0.7 | 39 | 20 | AA15623 | PCR primer for mo |
| C 32 | 21.8 | 0.7 | 39 | 20 | AA153160 | PCR primer #7 On |
| C 33 | 21.8 | 0.7 | 39 | 22 | AA154386 | Acetylated repeat med |
| C 34 | 21.8 | 0.7 | 48 | 24 | AB151939 | Human Snp oligonuc |
| C 35 | 21.8 | 0.7 | 51 | 22 | AA138644 | Human Snp oligonuc |
| C 36 | 21.8 | 0.7 | 51 | 23 | AA100653 | Human Snp oligonuc |
| C 37 | 21.8 | 0.7 | 52 | 16 | AA121611 | Staphylococcus aur |
| C 38 | 21.8 | 0.7 | 60 | 18 | AAV75963 | Human spliced tran |
| C 39 | 21.8 | 0.7 | 60 | 24 | ABN49878 | Aspergillus foot of |
| C 40 | 21.6 | 0.7 | 51 | 16 | AAV98582 | Aspergillus foot of |
| C 41 | 21.6 | 0.7 | 51 | 16 | AAV98581 | Human Snp oligonuc |
| C 42 | 21.6 | 0.7 | 51 | 22 | AA130771 | Human Snp oligonuc |
| C 43 | 21.6 | 0.7 | 51 | 22 | AA138424 | Human Snp oligonuc |
| C 44 | 21.6 | 0.7 | 60 | 24 | ABN42202 | Human spliced tran |
| C 45 | 21.6 | 0.7 | 60 | 24 | ABN47958 | Human spliced tran |

ALIGNMENTS

RESULT 1

AA146192/c

ID AA146192 standard; DNA: 45 bp.

AC AA146192;

XX

XX

DT 22-JUL-1997 (first entry)

XX

DE Primer for ribonuclease L cDNA amplification.

XX

KW Bovine; 2',5'-oligoadenylate acid synthase; plant

KW RNA virus; ribonuclease L; cucumber mosaic virus; primer, 1996; 88.

XX

OS Synthetic.

PN

PN W09638044-A1.

XX

PD 05 DEC-1996.

XX

FF 31 MAY-1996; 96WP 0101485.

XX

PR 08-MAR-1996; 96JP 0052010.

PR 31-MAY-1996; 96JP 0133741.

PR 01 NOV-1996; 96JP 0285401.

XX

XX (KIRI) KIRIN BEER KK.

XX

XX Ishida T., Iqawa T., Yoshioka M.

XX

XX WPI; 1997-044004/03.

XX

PT Plants resistant to attack by RNA viruses have


```

PR 21-APR-1998; 980S-0082614.
PR 23-NOV-1998; 980S-0109732.
PA (GENSET)
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX WPI; 2000 013267/01.
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome
XX
XX Claim 1; Page 458; 2745pp; English.
XX
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences; AAZ69579 to AAZ77440 represent amplification
XX primers for the biallelic markers. The biallelic markers of the
XX invention have a variety of uses; they can be used for high density
XX mapping of the human genome, and in complex association studies and
XX haplotyping studies which are useful in determining the genetic basis
XX for disease states. Compositions and methods of the invention can also
XX be useful for the identification of the targets for the development of
XX pharmaceutical agents and diagnostic methods, as well as the
XX characterisation of the differential efficacious responses to and side
XX effects from pharmaceutical agents acting on a disease as well as other
XX treatment.
XX N.B. The SEQ ID NOS 2852, 2913, 2974, 3015, 3096, 3157, 3227, 3297
XX and 3367, are not actually given a sequence in the Sequence Listing
XX from the present invention.
XX
XX Sequence 47 BP; 12 A; 9 C; 8 G; 18 T; 0 other.
XX
Query Match 0.8%; Score 24.8; DB 21; Length 41;
Best Local Similarity 72.7%; Pred. No. 4e+03;
Matches 32, Conservative 0; Mismatches 12, Indels 0, Gaps 0;
QY 2664 GATTATCATCCCATTTTAAAGACTGAGAACTGAGATGAGATGAGAG 2707
DB 4 GATTATTTCCCTCTTTTCAAAATCAGCAAGCTCAGGTTTAGAG 47
RESULT 7
AAL28761
ID AAL28761 standard; DNA; 51 BP.
AC AAL28761,
XX
XX 24-JAN-2002 (first entry)
XX
XX Human SNP oligonucleotide #1969.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;
XX cyclin; polymetase; oncogene; histone; kinase; colony stimulating factor;
XX complement related protein; cytochrome; kinesin; cytokine; interferon;
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX multifactorial disease; autoimmune disease; infection;
XX nervous system disease; ss.
XX
XX Homo sapiens.
XX
XX W0200147944-A2.
XX
XX 05-JUL-2001.
XX
XX 24-DEC-2000; 2000WO-0535498.
XX
XX 28-DEC-1999; 99US-0173419.
XX
XX 27-DEC-2000; 2000US-0173419.
XX
XX (CURA-) CURAGEN CORP.
XX
Shinkets RA, Leach M;
WPI; 2001-465210/50.
Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
oncogenes and histones, useful for diagnosing and treating, e.g.
cancer, autoimmune diseases and infections
Claim 1; Page 1944; 4143pp; English.
The present invention relates to oligonucleotides encoding polymorphic
variants of proteins related to amylases, amyloid proteins, angiotensin,
apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
histones, kinases, colony stimulating factors, complement related
proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
G-protein coupled receptors and thioesterases. The present sequence is
one such oligonucleotide. The oligonucleotides and the peptides encoded
by them may be used in the prevention, diagnosis and treatment of
diseases associated with inappropriate expression of the proteins listed
above. Disorders that may be prevented, diagnosed and/or treated include
multifactorial diseases with a genetic component, such as autoimmune
diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
systemic lupus erythematosus and Grave's disease), inflammation, cancer
(e.g. cancers of the bladder, brain, breast, colon and kidney,
leukaemia), diseases of the nervous system and an infection of pathogenic
organisms.
Sequence 51 BP; 22 A; 8 C; 9 G; 12 T; 0 other;
Query Match 0.8%; Score 24.6; DB 22; Length 51;
Best Local Similarity 70.2%; Pred. No. 4.8e+03;
Matches 33, Conservative 0; Mismatches 14, Indels 0; Gaps 0;
QY 2706 ATTTCCGAGACACACATTGATGAGAGAAAGCATAAACATCAAAATTA 2152
DB 5 ATTTGGAGGAAAAAAGACATGATTCAGCAACAAAGATGAATTA 51
RESULT 8
ABN35766
ID ABN35766 standard; DNA; 60 BP.
AC ABN35766;
XX
XX 15-JUL-2002 (first entry)
XX
XX Human spliced transcript detection oligonucleotide SEQ ID NO:6514.
XX
XX Human, mouse, rat, splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss
XX
XX Homo sapiens.
XX
XX W0200210449-A2.
XX
XX 07-FEB-2002.
XX
XX 20-JUL-2001; 2001WO-1801903.
XX
XX 24-JUL-2000; 2000US-221607P.
XX
XX 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
XX
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faidler S;
XX WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of
XX a genome, useful for detecting tissue-, pathology-, and
XX developmental-specific genes

```

XX Example 1: SEQ ID NO:14: 47pp: English.
 PS The present invention describes oligonucleotide libraries for detecting
 XX messenger RNAs that populate a (sub)transcriptome, where the
 CC (sub)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises
 CC several oligonucleotides, each capable of hybridizing selectively to a
 CC set of messenger RNAs transcribed from a given transcription unit of
 CC the genome, which encodes one or more messenger RNA splice variants.
 CC The oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterizing the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a
 CC particular biological or pathological state, and so allowing the
 CC detection of tissue- and pathology-specific genes such as those genes
 CC only expressed in specific tissue under a specific pathological
 CC condition; to detect developmental specific genes; and to detect RNA
 CC transcripts and splice variants of a transcriptome of a patient suffering
 CC from a particular disorder. AHN2753 to AHN59589 represent
 CC oligonucleotide sequences from rats, humans and mice, which are used in
 CC the exemplification of the present invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from Wipo
 CC at ftp.wipo.int/pub/published_pat_sequences.
 XX
 SQ Sequence: 60 BP; 15 A; 19 C; 10 G; 16 T; 0 other;

Query Match: 0.8%; Score: 24.6; DB: 24; Length: 60;
 Best Local Similarity: 65.5%; Pred. No.: 5.3e+04;
 Matches: 46; Conservative: 0; Mismatches: 19; Indels: 0; Gaps: 0.
 QY 2176 TTTCACAGACATCTTCAGATCTGATCTATCTACACAAACACACACAC 2330
 DB 6 TTCTGAGAGACTTCAGATCTGATCTATCTACACAAACACACACAC 60
 RESULT 9
 AHN47478
 ID AHN47478 standard; DNA: 60 BP.
 AC AHN47478;
 XX
 DT 15 JUL 2002 (first entry)
 XX
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:20126.
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.
 XX Homo Sapiens.
 XX W0200210449 A2.
 XX
 DT 07 FEB 2002
 XX
 DE 20 JUL 2001; 2001WO 180190A.
 XX
 DE 28 JUL 2000; 2000US 221607P.
 PR 02 MAY 2001; 2001US 267724P.
 XX
 XX (COMP) COMPUGEN INC.
 XX Shoshan A. Wasserman A. Mintz E. Mintz L. Falqier S.
 XX WPI; 2002 257483/40.
 XX
 PT New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of
 PT a genome, useful for detecting tissue-, pathology-, and
 PT developmental specific genes.

XX Example 1: SEQ ID NO:16: 47pp: English.
 PS the present invention describes oligonucleotide libraries for detecting
 XX messenger RNAs that populate a (sub)transcriptome, where the
 CC (sub)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises
 CC several oligonucleotides, each capable of hybridizing selectively to a
 CC set of messenger RNAs transcribed from a given transcription unit of
 CC the genome, which encodes one or more messenger RNA splice variants.
 CC The oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterizing the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a
 CC particular biological or pathological state, and so allowing the
 CC detection of tissue- and pathology-specific genes such as those genes
 CC only expressed in specific tissue under a specific pathological
 CC condition; to detect developmental specific genes; and to detect RNA
 CC transcripts and splice variants of a transcriptome of a patient suffering
 CC from a particular disorder. AHN2753 to AHN59589 represent
 CC oligonucleotide sequences from rats, humans and mice, which are used in
 CC the exemplification of the present invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from Wipo
 CC at ftp.wipo.int/pub/published_pat_sequences.
 XX
 SQ Sequence: 60 BP; 14 A; 17 C; 8 G; 22 T; 0 other;

Query Match: 0.8%; Score: 24.4; DB: 24; Length: 60;
 Best Local Similarity: 74.8%; Pred. No.: 6.1e+04;
 Matches: 31; Conservative: 0; Mismatches: 11; Indels: 0; Gaps: 0.
 QY 2866 TCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 2907
 DB 7 TCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 48
 RESULT 10
 AHN409437C
 ID AHN40943 standard; DNA: 60 BP.
 AC AHN40943;
 XX
 DT 15 JUL 2002 (first entry)
 XX
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:14094.
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.
 XX Homo Sapiens.
 XX W0200210449 A2.
 XX
 DT 07 FEB 2002
 XX
 DE 20 JUL 2001; 2001WO 180190A.
 XX
 DE 28 JUL 2000; 2000US 221607P.
 PR 02 MAY 2001; 2001US 267724P.
 XX
 XX (COMP) COMPUGEN INC.
 XX Shoshan A. Wasserman A. Mintz E. Mintz L. Falqier S.
 XX WPI; 2002 257483/40.
 XX
 PT New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of
 PT a genome, useful for detecting tissue-, pathology-, and
 PT developmental specific genes.

XX Example 1: SEQ ID 13691; 47pp; English.
 XX
 CC The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises
 CC several oligonucleotides, each capable of hybridizing selectively to a
 CC set of messenger RNAs transcribed from a given transcription unit of
 CC the genome, which encodes one or more messenger RNA splice variants.
 CC The oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterizing the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC libraries to detect transcripts of a sub-transcriptome under a
 CC particular biological or pathological state, and so allowing the
 CC detection of tissue- and pathology-specific genes such as those genes
 CC only expressed in specific tissue under a specific pathological
 CC condition; to detect developmental specific genes; and to detect RNA
 CC transcripts and splice variants of a transcriptome of a patient suffering
 CC from a particular disorder. ABN27253 to ABN59589 represent
 CC oligonucleotide sequences from rats, humans and mice, which are used in
 CC the exemplification of the present invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SO Sequence 60 BP; 11 A, 18 C, 13 G, 18 T, 0 other.

Query Match 0.8%; Score 23.4; DB 24; Length 60;
 Best Local Similarity 67.3%; Pred. No. 1.2e+04;
 Matches 33; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 2677 ATTGAACACTGAGAACCTTCAGACTCAGAGAGCTGTGACCTACTGGCC 2725
 DB 59 AGTTACAGATGGGAATACTAGAGGCTTGAAGAAGATCTATGATGCTG 11

RESULT 11
 ABN48713
 ID ABN48713 standard; DNA; 60 BP.
 AC ABN48713;

15-JUL-2002 (first entry)

Human spliced transcript detection oligonucleotide SEQ ID NO:21461.

Human; mouse; rat; splice transcript; detection; RNA transcript;
 splice variant, transcriptome, oligonucleotide library; ss

Homo sapiens.

W0200210449-A2.

07-FEB-2002.

20-JUL-2001; 2001WO-1B01903.

28-JUL-2000; 2000RS-221607P

02-MAY-2001; 2001US-287724P.

(COMP-) COMPUGEN INC.

Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

WPI; 2002-257383/30.

New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of
 PT a genome, useful for detecting tissue-, pathology-, and
 PT developmental-specific genes

XX

Example 1: SEQ ID 21461; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises
 CC several oligonucleotides, each capable of hybridizing selectively to a
 CC set of messenger RNAs transcribed from a given transcription unit of
 CC the genome, which encodes one or more messenger RNA splice variants.
 CC The oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterizing the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC libraries to detect transcripts of a sub-transcriptome under a
 CC particular biological or pathological state, and so allowing the
 CC detection of tissue- and pathology-specific genes such as those genes
 CC only expressed in specific tissue under a specific pathological
 CC condition; to detect developmental specific genes; and to detect RNA
 CC transcripts and splice variants of a transcriptome of a patient suffering
 CC from a particular disorder. ABN27253 to ABN59589 represent
 CC oligonucleotide sequences from rats, humans and mice, which are used in
 CC the exemplification of the present invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX

SO Sequence 60 BP; 22 A, 14 C, 14 G, 10 T; 0 other;

Query Match 0.8%; Score 23.2; DB 24; Length 60;
 Best Local Similarity 70.5%; Pred. No. 1.4e+04;
 Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 1638 GAGTCCACGACGAGCTCAGAGAGATAGAGAGACCTTCGACCG 1681

DB 1 GATATCCATAGGAGTAAACCAACAACTTCAGAGAGCTAGGACTG 44

RESULT 12
 ABN36051/C
 ID ABN36051 standard; DNA; 60 BP.
 AC ABN36051;

15-JUL-2002 (first entry)

Human spliced transcript detection oligonucleotide SEQ ID NO:8799.

Human; mouse; rat; splice transcript; detection; RNA transcript;
 splice variant, transcriptome, oligonucleotide library; ss.

Homo sapiens.

W0200210449-A2.

07-FEB-2002.

20-JUL-2001; 2001WO-1B01903.

28-JUL-2000; 2000RS-221607P

02-MAY-2001; 2001US-287724P.

(COMP-) COMPUGEN INC.

Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

WPI; 2002-257383/30.

New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of
 PT a genome, useful for detecting tissue-, pathology-, and
 PT developmental-specific genes

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

nm nucleic nucleic search, using sw model

Run on April 16, 2003, 22:40:29 : Search time 8422 Seconds
(without alignments)
10117.907 Million cell updates/sec

Title: US 09 954 679-3
Perfect score: 2928
Sequence: 1 aatcccaattacactcaad.....gggcactggatgcattgaatt 2928

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2064640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 897812

Minimum DB seq length: 0
Maximum DB seq length: 60

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank

- 1: qb ba:*
- 2: qb hta:*
- 3: qb in:*
- 4: qb cm:*
- 5: qb ov:*
- 6: qb pat:*
- 7: qb ph:*
- 8: qb pl:*
- 9: qb pr:*
- 10: qb ro:*
- 11: qb sts:*
- 12: qb sy:*
- 13: qb un:*
- 14: qb vi:*
- 15: em ba:*
- 16: em fun:*
- 17: em hum:*
- 18: em in:*
- 19: em mu:*
- 20: em om:*
- 21: em or:*
- 22: em ov:*
- 23: em pat:*
- 24: em ph:*
- 25: em pl:*
- 26: em ro:*
- 27: em sts:*
- 28: em un:*
- 29: em vi:*
- 30: em hta: hum:*
- 31: em hta: inv:*
- 32: em hta: of her:*
- 33: em hta: mus:*
- 34: em hta: pin:*
- 35: em hta: rod:*
- 36: em hta: mam:*
- 37: em hta: vrt:*
- 38: em sy:*
- 39: em hta: hum:*
- 40: em hta: mus:*
- 41: em hta: other:*

Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 25 | 0.9 | 48 | 6 | AR016283 |
| 2 | 24 | 0.8 | 54 | 6 | AR064408 |
| 3 | 22.6 | 0.8 | 47 | 6 | A21609 |
| 4 | 22.4 | 0.8 | 58 | 6 | AX481765 |
| 5 | 22.4 | 0.8 | 59 | 6 | AX011418 |
| 6 | 22.4 | 0.8 | 60 | 6 | AR201911 |
| 7 | 22.2 | 0.8 | 50 | 9 | HSEDA05 |
| 8 | 22.2 | 0.8 | 60 | 6 | AR170294 |
| 9 | 22.2 | 0.8 | 60 | 6 | AX007121 |
| 10 | 22.2 | 0.8 | 60 | 6 | E51067 |
| 11 | 22 | 0.8 | 54 | 10 | AF224157 |
| 12 | 21.8 | 0.7 | 39 | 6 | AR151069 |
| 13 | 21.8 | 0.7 | 49 | 6 | E15325 |
| 14 | 21.8 | 0.7 | 51 | 6 | AX116417 |
| 15 | 21.8 | 0.7 | 51 | 6 | AX165449 |
| 16 | 21.6 | 0.7 | 51 | 6 | AX3564 |
| 17 | 21.6 | 0.7 | 51 | 6 | AX5565 |
| 18 | 21.6 | 0.7 | 51 | 6 | AR019428 |
| 19 | 21.6 | 0.7 | 51 | 6 | AR019429 |
| 20 | 21.6 | 0.7 | 51 | 6 | AX116097 |
| 21 | 21.4 | 0.7 | 51 | 6 | AX161191 |
| 22 | 21.4 | 0.7 | 51 | 10 | AF428711 |
| 23 | 21.4 | 0.7 | 54 | 9 | S60665 |
| 24 | 21.4 | 0.7 | 60 | 6 | AX481481 |
| 25 | 21.2 | 0.7 | 51 | 6 | AX118093 |
| 26 | 21.2 | 0.7 | 51 | 6 | AX190126 |
| 27 | 21.2 | 0.7 | 51 | 6 | AX204485 |
| 28 | 21 | 0.7 | 57 | 3 | AF049618 |
| 29 | 21 | 0.7 | 60 | 6 | AR051681 |
| 30 | 20.8 | 0.7 | 50 | 9 | AF057518 |
| 31 | 20.8 | 0.7 | 51 | 6 | AX158446 |
| 32 | 20.8 | 0.7 | 51 | 9 | AF079028 |
| 33 | 20.8 | 0.7 | 54 | 9 | AF078972 |
| 34 | 20.8 | 0.7 | 54 | 6 | AX253482 |
| 35 | 20.8 | 0.7 | 59 | 6 | AX554804 |
| 36 | 20.8 | 0.7 | 60 | 6 | AR160248 |
| 37 | 20.6 | 0.7 | 45 | 6 | A05547 |
| 38 | 20.6 | 0.7 | 45 | 6 | AR001640 |
| 39 | 20.6 | 0.7 | 45 | 6 | AX448220 |
| 40 | 20.6 | 0.7 | 45 | 6 | 109087 |
| 41 | 20.6 | 0.7 | 51 | 6 | AX158947 |
| 42 | 20.6 | 0.7 | 54 | 6 | A66662 |
| 43 | 20.6 | 0.7 | 54 | 6 | A66663 |
| 44 | 20.6 | 0.7 | 57 | 6 | AX257322 |
| 45 | 20.4 | 0.7 | 47 | 6 | AX458041 |

ALIGNMENTS

| RESULT 1 | AR016283 | 48 bp | DNA | Insertion | Pat. No. 5776690 |
|------------|--|------------|-----|-----------|------------------|
| LOCUS | Sequence 6 from patent US 5776690 | | | | |
| DEFINITION | Sequence 6 from patent US 5776690 | | | | |
| ACCESSION | AR016283 | | | | |
| VERSION | AR016283.1 | GI:5972560 | | | |
| KEYWORDS | | | | | |
| SOURCE | Unknown | | | | |
| ORGANISM | Unknown | | | | |
| REFERENCE | 1 (bases 1 to 48) | | | | |
| AUTHORS | Vojdani, A. and Mordechai, E. | | | | |
| TITLE | Detection of chronic fatigue syndrome by decreased levels of RNAse | | | | |
| JOURNAL | 1. inhibitor mRNA | | | | |
| | Patent: US 5776690-A 6 07 JUN 1998 | | | | |

```

FEATURES
  source
    location/Qualifiers
    1..48
    /organism="unknown"
  BASE COUNT
    14 a 11 c 12 g 11 t
  ORIGIN

Query Match
  Best Local Similarity 0.9%; Score 25; DB 6; Length 48;
  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 638 GGACAGTAGAGTCTTCAGCAATTC 662
Db 1 GGACAGTAGAGTCTTCAGCAATTC 25

RESULT 2
LOCUS AR064498 54 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 71 from patent US 5847096.
ACCESSION AR064498
VERSION AR064498 1 GI:5993805
KEYWORDS
SOURCE
  ORGANISM
    Unknown.
    Unclassified.
  REFERENCE
    1 (bases 1 to 54)
    Schubert M., Harmison G G II, Chen, C.-J., and Banerjee, A.
    DNA constructs encoding CD4 fusion proteins
    JOURNAL Patent: US 5847096-A 71 08-DEC-1998;
  FEATURES
    location/Qualifiers
    1..54
    /organism="unknown"
  BASE COUNT
    14 a 18 c 10 g 12 t
    ORIGIN

Query Match
  Best Local Similarity 0.8%; Score 23; DB 6; Length 54;
  Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 910 AATCATATGCGCAAAAGACACTGCTGCTGCTGTGA 948
Db 40 AGTCGCTGAGGACCAACAGCAGTGGGTCTTGCTGATGA 2

RESULT 3
LOCUS A21609/c 37 bp DNA linear PAT 07-JUL-1994
DEFINITION oligonucleotide.
ACCESSION A21609
VERSION A21609 1 GI:583606
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct.
    synthetic construct.
    artificial sequences.
  FEATURES
    location/Qualifiers
    1..37
    /organism="synthetic construct"
    /db_xref="taxon:32630"
  BASE COUNT
    6 a 5 c 4 g 22 t
    ORIGIN

Query Match
  Best Local Similarity 0.8%; Score 22.6; DB 6; Length 37;
  Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2020 TGTATGAAAAAATGAATAGCTTTTATGAAAAAGA 2056
Db 37 TGTATGACAAAAAAGAAAAAGTGTCTATGACAAAAA 1

RESULT 4
LOCUS AX381765/c 58 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 703 from patent WO0212280.
ACCESSION AX381765
VERSION AX381765.1 GI:19576587
KEYWORDS
SOURCE
  ORGANISM
    human.
    Homo sapiens
    Fukuyota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
    Mammalia; Eutheria; Primates, Catarrhini, Hominoidea; Homo.
  REFERENCE
    1
    Pyle, P. A., Xu, T. and Secrist, H.
    Compositions and methods for the therapy and diagnosis of colon
    cancer
    Patent: WO 0212280-A 703 14-FEB 2002;
    CORIXA CORPORATION (US)
  FEATURES
    location/Qualifiers
    1..58
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
  BASE COUNT
    0 a 8 c 5 g 45 t
    ORIGIN

Query Match
  Best Local Similarity 0.8%; Score 22.4; DB 6; Length 58;
  Matches 35; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 2110 GCGAGACACATTGATCAAGAAAGCATAAAAATTCAGATCAATTAATAATTCGACACC 2165
Db 56 GCGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGGGG 1

RESULT 5
LOCUS AX011418 59 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 95 from Patent WO9555907.
ACCESSION AX011418
VERSION AX011418.1 GI:9997968
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct.
    synthetic construct.
    artificial sequences.
  REFERENCE
    1 (bases 1 to 59)
    Koetter, P., Ertan, K. D. and Diu-Herard, A.
    Method for screening antimycotic substances using essential genes
    from S. Cervisiae
    Patent: WO 9555907-A 95 04-NOV-1999;
    KOETTER PETER (DE); FNTIAN KAPL DIETER (DE); DIU HERARD ANITA
    (FR); HOECHST MARION ROUSSEL INC (FR)
  JOURNAL
  FEATURES
    location/Qualifiers
    1..59
    /organism="synthetic construct"
    /db_xref="taxon:32630"
    /note="primer YDR499w-S1"
  BASE COUNT
    16 a 11 c 18 g 14 t
    ORIGIN

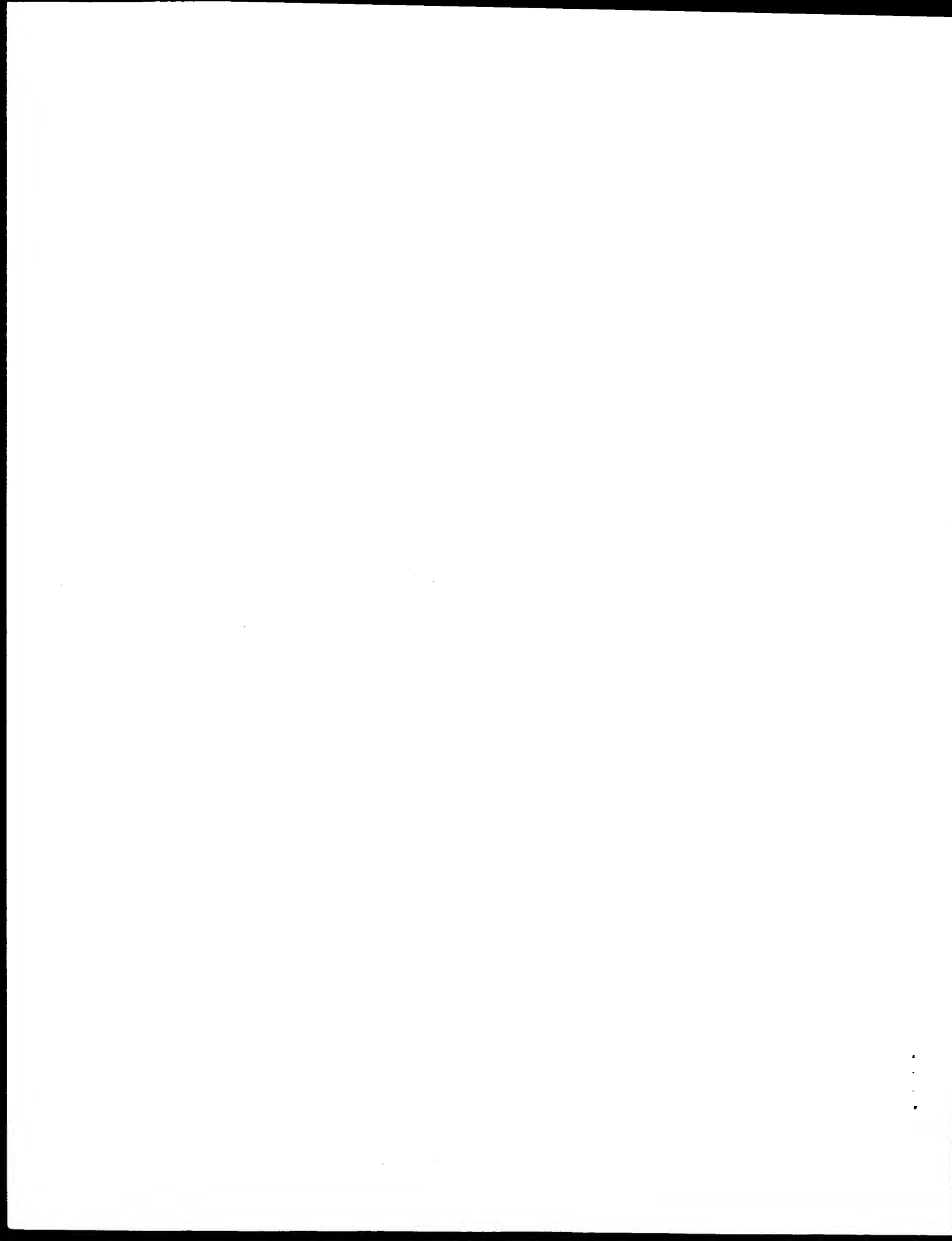
Query Match
  Best Local Similarity 0.8%; Score 22.4; DB 6; Length 59;
  Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1745 GAAGAGGAGGCTCAACTTCTCCAGATGAGGAACTAAAG 1784
Db 10 GAAGAGGAGGCTCAACTTCTCCAGATGAGGAACTAAAG 49

RESULT 6
LOCUS AR201911/c 60 bp DNA linear PAT 20-APR 2002
DEFINITION Sequence 14 from patent US 6361943.
ACCESSION AR201911
VERSION AR201911.1 GI:20256450
KEYWORDS
SOURCE
  ORGANISM
    Unknown.
    Unknown.

```


| | | | |
|----------------------|--|---------------------------------|--|
| | 1 | (bases 1 to 60) | |
| REFERENCE AUTHORS | Erhard,K.,and Chrithiane,S. | | |
| TITLE | Novel Escherichia coli/host vector system based on selection not relying on antibiotic by complementing auxotrophy | | |
| JOURNAL | PATENT JP 2000050888-A 7 22-FEB-2000; | | |
| COMMENT | ROCHE DIAGNOSTICS GMBH | | |
| | OS Artificial Sequence | | |
| PN | JP 2000050888-A/7 | | |
| PD | 22-FEB-2000 | | |
| PP | 15-JUL-1999 JP 1999202303 | | |
| PR | 15-JUL-1998 EP 98113156.8;09-OCT-1998 HP 98119078.8 PI | | |
| PC | C12N15/09,C12N1/21,C12P4/02//(C12N1/21,C12R1:19),(C12P21/02, | | |
| CC | C12N15/00 | | |
| FH | Key | Location/Qualifiers | |
| FT | source | location/Qualifiers | |
| | 1..60 | /organism='Artificial Sequence' | |
| | 1..60 | /db_xref='taxon:32630' | |
| BASE COUNT | 19 A 14 C 13 G 14 T | | |
| ORIGIN | | | |
| | Query Match Score 22.2; DH 6; length 60; | | |
| Matches | 33, Conservative 0; Mismatches 18; Indels 0; Gaps 0; | | |
| OY_1449 | GAGGGGAAGTGTGGAAGAATGAGGAGATGTAATTGCCCGAAATGCCTGT 1499 | | |
| Dn | I | | |
| Db | 54 GATCATCAAGCTGTCAAACATGAGGGGGCCCATATGCGCTATAIGGCCTTT 4 | | |
| RESULT 11 | | | |
| AF224157/c | | | |
| LOCUS | | | |
| DEFINITION | Af224157 Mus musculus GBTCRI10.53 T cell receptor beta-chain CDR3 gene, | | |
| ACCESION | | | |
| VERSION | | | |
| KEYWORDS | | | |
| SOURCE | | | |
| ORGANISM | | | |
| REFERENCE | | | |
| AUTHORS | | | |
| TITLE | | | |
| JOURNAL | | | |
| REFERENCE | | | |
| AUTHORS | | | |
| TITLE | | | |
| JOURNAL | | | |
| FEATURES | | | |
| source | | | |
| | 1..54 | /organism='Mus musculus' | |
| | /strain='C57BL/6J' | | |
| | /db_xref='taxon:10090' | | |
| | /clone='GBTCRI0.53' | | |
| | 'cell_line'-'T cell line specific for HSV-1 qB498-505 | | |
| | determinant' | | |
| | <I>'.'..'54 | | |
| | /note='TCRBV10' | | |
| | /codon_start=1 | | |
| | /product='T cell receptor beta chain CDR3' | | |
| | /protein_id='AAF33304.1' | | |



| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|---------------------|--------------------|
| c 1 | 22.4 | 0.8 | 58 | 10 | US-09-919-580-703 | Sequence 703, Appl |
| c 2 | 22.4 | 0.8 | 63 | 9 | US-10-238-970-14 | Sequence 14, Appl |
| c 3 | 22.4 | 0.8 | 63 | 12 | US-10-046-723-14 | Sequence 14, Appl |
| c 4 | 22.2 | 0.8 | 51 | 9 | US-09-764-872-151 | Sequence 151, Appl |
| c 5 | 21.8 | 0.7 | 60 | 7 | US-08-781-986A-1652 | Sequence 1652, Ap |
| c 6 | 21.6 | 0.7 | 60 | 9 | US-09-362-286-22 | Sequence 22, Appl |
| c 7 | 21.4 | 0.7 | 60 | 10 | US-09-919-580-419 | Sequence 419, Appl |
| c 8 | 21.2 | 0.7 | 52 | 7 | US-08-781-986A-5071 | Sequence 5071, Ap |
| c 9 | 20.8 | 0.7 | 59 | 10 | US-09-855-159-2 | Sequence 2, Appl |
| c 10 | 20.8 | 0.7 | 59 | 12 | US-10-013-737-12 | Sequence 12, Appl |
| c 11 | 20.6 | 0.7 | 57 | 7 | US-08-781-986A-3384 | Sequence 3384, Ap |
| c 12 | 20.4 | 0.7 | 57 | 9 | US-10-199-430-12 | Sequence 12, Appl |
| c 13 | 20.4 | 0.7 | 57 | 9 | US-10-199-334-12 | Sequence 12, Appl |
| c 14 | 20.2 | 0.7 | 47 | 9 | US-09-758-017A-18 | Sequence 18, Appl |
| c 15 | 20.2 | 0.7 | 51 | 10 | US-09-790-417-241 | Sequence 231, Appl |
| c 16 | 20 | 0.7 | 40 | 10 | US-09-947-305-3 | Sequence 3, Appl |
| c 17 | 20 | 0.7 | 46 | 10 | US-09-827-289-25 | Sequence 25, Appl |
| c 18 | 20 | 0.7 | 53 | 10 | US-09-912-787-38 | Sequence 38, Appl |
| c 19 | 20 | 0.7 | 53 | 12 | US-10-014-326-24 | Sequence 24, Appl |

CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/228,070
FILING DATE: 27-Aug-2002
CLASSIFICATION: (D) REFERENCE: 2002-1108/LC/01416
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10/046,722
FILING DATE: 17-Jan-02
APPLICATION NUMBER: 09/284,627
FILING DATE: 02-Jun-99
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 60
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
FEATURE:
OTHER INFORMATION: has a sequence partly
complementary to SEQ ID NO: 17
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-228-070-14
Query Match 0.8%; Score 22.4; DB 9; Length 60;
Best Local Similarity 66.7%; Pred. No. 1.2e+04;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 2111 GGAGACACATTCATGACAAAGCAATAAAAGATGAAATTTAAAAATT 2158
DB 55 GGGAGGTCATTAAAAAAGCAATAAAAGATGAAATTTAAAAATT 8
RESULT 3
US-10-046-722-14/c
Sequence 14, Application US/10046722
Patent No. US2002072087A1
GENERAL INFORMATION:
APPLICANT: Hiroshi YANAGAWA et al.
TITLE OF INVENTION: Molecule Assigning Genotype To Phenotype And Use Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Wondoroth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/046,722
FILING DATE: 17-Jan-2002
CLASSIFICATION: (D) REFERENCE: 2001-1211/LC/01416
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/284,627
FILING DATE: 02-Jun-99
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

LENGTH: 60
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: synthetic DNA
FEATURE:
OTHER INFORMATION: has a sequence partly
complementary to SEQ ID NO: 17
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10 046-722-14
Query Match 0.8%; Score 22.4; DB 12; Length 60;
Best Local Similarity 66.7%; Pred. No. 1.2e+04;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 2111 GGAGACACATTCATGACAAAGCAATAAAAGATGAAATTTAAAAATT 2158
DB 55 GGGAGGTCATTAAAAAAGCAATAAAAGATGAAATTTAAAAATT 8
RESULT 4
US-09-764-872-151
Sequence 151, Application US/09764872
Publication No. US20030050231A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA125
CURRENT APPLICATION NUMBER: US/09/764,872
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 957
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 151
LENGTH: 51
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-872-151
Query Match 0.8%; Score 22.2; DB 9; Length 51;
Best Local Similarity 77.1%; Pred. No. 1.2e+04;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1750 GTGGGTCACACATTCACAGATGAGGAACTAAGG 1784
DB 1 GATGTTCTACCTTTTTCAGATGAGGAACTAAGG 35
RESULT 5
US-08-781-986A-1652/c
Sequence 1652, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44M storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MS-DOS version 6.0
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435


```

1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER:
3 FILING DATE:
4 ATTORNEY/AGENT INFORMATION:
5 NAME: Benson, Bob
6 REGISTRATION NUMBER: 40,446
7 REFERENCE/DOCKET NUMBER: PH248PP
8 TELECOMMUNICATION INFORMATION:
9 TELEPHONE: (301) 309-8504
10 TELEFAX: (301) 309-8512
11 INFORMATION FOR SEQ ID NO: 1652:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 60 base pairs
14 TYPE: nucleic acid
15 STRANDEDNESS: double
16 TOPOLOGY: linear
17 US 09 781 986A 1652

Query Match 0.7% Score 21.8; DB 7; Length 60;
Best Local Similarity 78.8%; Pred. No. 1.8e+04;
Matches 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2868 ATTATTCATTCAGTATTTATGACATCTACT 2900
DB 45 ATACCTTCATATGTTATTTATGTCATGTAGT 3

RESULT 6
US 09 362 286 22
1 SEQUENCE 22, Application US/09/362,286
2 Publication No. US20020197706A1
3 GENERAL INFORMATION:
4 APPLICANT: Nadkarni, Anupama K.
5 APPLICANT: Truchardt, Joshua
6 TITLE OF INVENTION: Expression of G Protein-Coupled Receptors with Altered
7 FILE REFERENCE: CPl 099
8 CURRENT APPLICATION NUMBER: US/09/362,286
9 CURRENT FILING DATE: 1999-07-27
10 NUMBER OF SEQ ID NOS: 47
11 SOFTWARE: Patent In Ver. 2.0
12 SEQ ID NO 22
13 LENGTH: 60
14 TYPE: DNA
15 ORGANISM: Artificial Sequence
16 FEATURE:
17 OTHER INFORMATION: Description of Artificial Sequence:
18 OTHER INFORMATION: oligonucleotide
19 US 09-362 286 22

Query Match 0.7% Score 21.6; DB 9; Length 60;
Best Local Similarity 60.0%; Pred. No. 2e+04;
Matches 36; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1537 GTGTGATACACGACACAGATCTGACACACAAACATCTTAATAGATTCTTAAGAAAGC 1596
DB 1 CTTCGATCCAAACACAACTCTCTACCAACACACATTAACAATAATTCAGTGTAGC 60

RESULT 7
US 09 919 580 419/c
1 SEQUENCE 419, Application US/09919580
2 Patent No. US20020110842A1
3 GENERAL INFORMATION:
4 APPLICANT: Pyle, Ruth
5 APPLICANT: Xu, Jianqichun
6 APPLICANT: Secriest, Heather
7 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
8 FILE REFERENCE: 210121.552
9 CURRENT APPLICATION NUMBER: US/09/919,580
10 CURRENT FILING DATE: 2001 07-30
11 NUMBER OF SEQ ID NOS: 944

```

```

1 SOFTWARE: FastSeq for Windows Version 4.0
2 SEQ ID NO 419:
3 LENGTH: 60
4 TYPE: DNA
5 ORGANISM: Homo sapiens
6 FEATURE:
7 NAME/KEY: nisc_feature
8 LOCATION: 54
9 OTHER INFORMATION: n = A,L,C or G
10 US-09-919-580-419

Query Match 0.7% Score 21.4; DB 10; Length 60;
Best Local Similarity 60.7%; Pred. No. 2.4e+04;
Matches 34; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 2110 GCGAGAACACATTCATGACAGAAAGCAATAAAACATCAAAATTAATAATTCGACACAC 2105
DB 56 GGNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 8
US-08-781-986A-5071/c
1 SEQUENCE 5071, Application US/98781986A
2 Publication No. US20030054446A1
3 GENERAL INFORMATION:
4 APPLICANT: Charles Kunsch
5 TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
6 NUMBER OF SEQUENCES: 5255
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Human Genome Sciences, Inc.
9 STREET: 9410 Key West Avenue
10 CITY: Rockville
11 STATE: Maryland
12 COUNTRY: USA
13 ZIP: 20850
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
16 COMPUTER: HP Vectra 486/33
17 OPERATING SYSTEM: MSDOS version 6.2
18 SOFTWARE: ASCII Text
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/08/781,986A
21 FILING DATE:
22 CLASSIFICATION: 435
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER:
25 FILING DATE:
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Benson, Bob
28 REGISTRATION NUMBER: 40,446
29 REFERENCE/DOCKET NUMBER: PH248PP
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: (301) 309-8504
32 TELEFAX: (301) 309-8512
33 INFORMATION FOR SEQ ID NO: 5071:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 52 base pairs
36 TYPE: nucleic acid
37 STRANDEDNESS: double
38 TOPOLOGY: linear
39 US-08-781-986A-5071

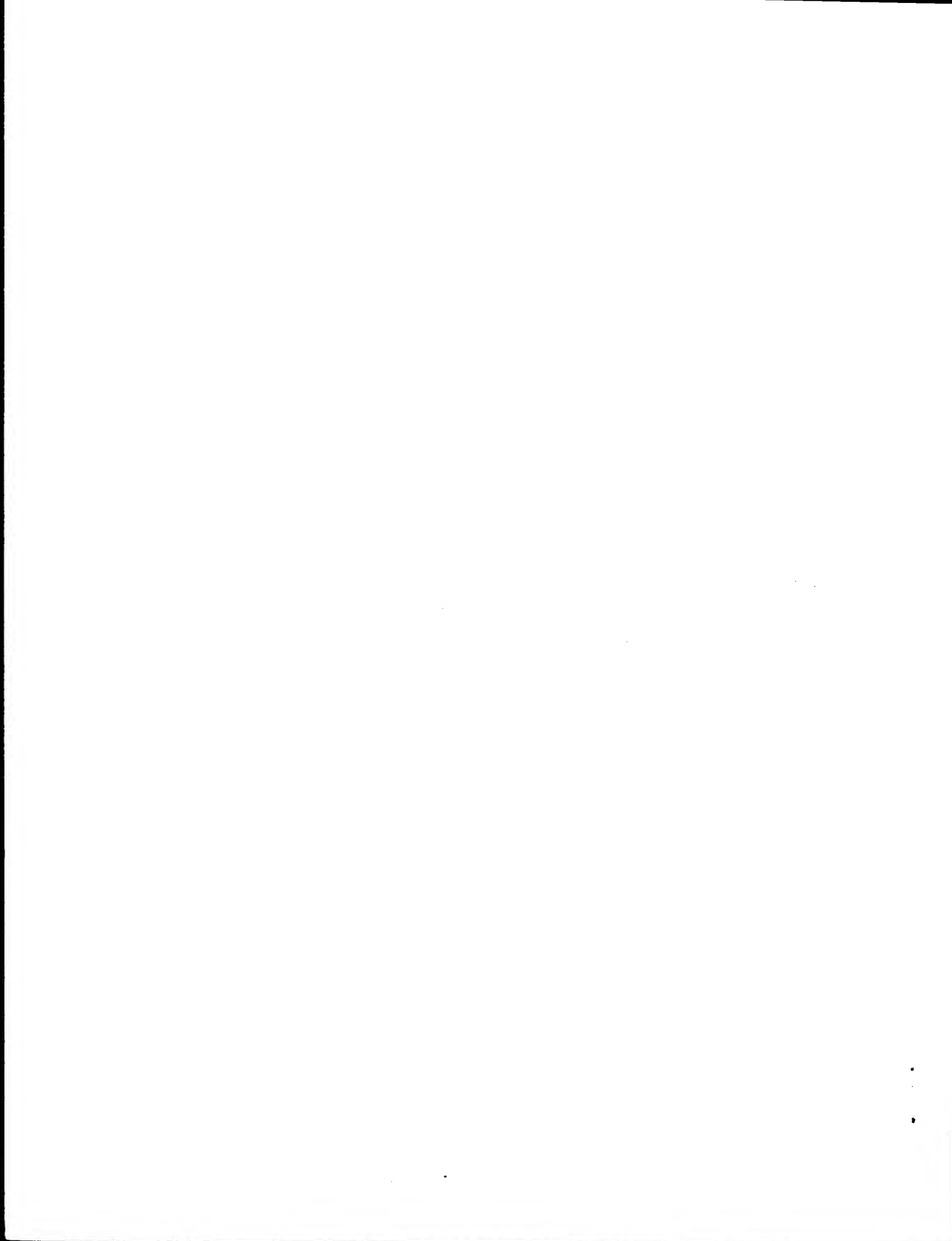
Query Match 0.7% Score 21.2; DB 7; Length 52;
Best Local Similarity 69.0%; Pred. No. 2.4e+04;
Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2839 AAAACATATATAGGGTTCAGGAATCTCATTCATTCATTCATCA 2880
DB 46 AAAACCAITATAGCTGTATAGGAATATCAATCTGTTATTCATCA 5

RESULT 9
US-09-855-159-2/c

```

[illegible]



Genome version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

cm nucleic nucleic search, using sw model

Run on: April 16, 2003, 22:41:29 : Search time 4479 Seconds
(without alignments)
10587.271 Million cell updates/sec

Title: us-09-954 679-3

Perfect score: 2928

Sequence: 1 aatcccaattaccactcaaa.....gggcactggatgcatdaatt 2928

Scoring table: IDENTITY_NIC

Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 146654

Minimum DB seq length: 0

Maximum DB seq length: 60

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: EST:

| | |
|-----|----------------|
| 1: | cm_estba:* |
| 2: | cm_esthum:* |
| 3: | cm_estin:* |
| 4: | cm_estma:* |
| 5: | cm_estow:* |
| 6: | cm_estpl:* |
| 7: | cm_estro:* |
| 8: | cm_estre:* |
| 9: | qb_est1:* |
| 10: | qb_est2:* |
| 11: | qb_est3:* |
| 12: | qb_est4:* |
| 13: | qb_est5:* |
| 14: | qb_est6:* |
| 15: | cm_estlum:* |
| 16: | cm_estom:* |
| 17: | qb_oss:* |
| 18: | cm_oss_hum:* |
| 19: | cm_oss_inv:* |
| 20: | cm_oss_pln:* |
| 21: | cm_oss_vrt:* |
| 22: | cm_oss_fun:* |
| 23: | cm_oss_mam:* |
| 24: | cm_oss_mus:* |
| 25: | cm_oss_othel:* |
| 26: | cm_oss_pro:* |
| 27: | cm_oss_rtd:* |

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 27.8 | 0.9 | 58 | 14 | H05434.y180h11.s1 |
| 2 | 27.4 | 0.9 | 58 | 17 | BH623868 |
| 3 | 26.6 | 0.9 | 60 | 14 | BH5541 |
| 4 | 26.6 | 0.9 | 52 | 9 | AA782923 |
| 5 | 25.6 | 0.9 | 59 | 14 | N24179 |
| 6 | 25.2 | 0.9 | 55 | 13 | BC943565 |

| | | | | | | |
|---|----|------|-----|----|----|-----------|
| c | 7 | 24.6 | 0.8 | 51 | 9 | AA417159 |
| | 8 | 24.4 | 0.8 | 60 | 17 | A1524624 |
| | 9 | 24.2 | 0.8 | 60 | 17 | CR594721 |
| | 10 | 24 | 0.8 | 60 | 13 | B6522115 |
| | 11 | 23.8 | 0.8 | 54 | 12 | B6671284 |
| | 12 | 23.8 | 0.8 | 59 | 13 | B1246744 |
| | 13 | 23.8 | 0.8 | 60 | 13 | B1148041 |
| | 14 | 23.2 | 0.8 | 49 | 9 | AA522891 |
| | 15 | 23.2 | 0.8 | 54 | 10 | AN082814 |
| | 16 | 23 | 0.8 | 58 | 17 | BH842562 |
| | 17 | 22.6 | 0.8 | 55 | 9 | A1123105 |
| c | 18 | 22.4 | 0.8 | 49 | 17 | A7957556 |
| c | 19 | 22.4 | 0.8 | 53 | 12 | BH650156 |
| c | 20 | 22.4 | 0.8 | 57 | 17 | BH751620 |
| c | 21 | 22.4 | 0.8 | 58 | 17 | BH849944 |
| c | 22 | 22.4 | 0.8 | 58 | 17 | BH850471 |
| c | 23 | 22.4 | 0.8 | 60 | 10 | BH435785 |
| c | 24 | 22 | 0.8 | 46 | 14 | N44913 |
| c | 25 | 22 | 0.8 | 56 | 2 | HS0001867 |
| c | 26 | 21.8 | 0.7 | 50 | 9 | A2103212 |
| c | 27 | 21.8 | 0.7 | 52 | 14 | B45784 |
| c | 28 | 21.8 | 0.7 | 55 | 12 | BH95446 |
| c | 29 | 21.8 | 0.7 | 56 | 10 | AV964895 |
| c | 30 | 21.8 | 0.7 | 57 | 10 | AM694683 |
| c | 31 | 21.8 | 0.7 | 58 | 17 | BH627964 |
| c | 32 | 21.8 | 0.7 | 59 | 13 | BH187386 |
| c | 33 | 21.8 | 0.7 | 59 | 17 | A2502276 |
| c | 34 | 21.6 | 0.7 | 55 | 12 | B65019461 |
| c | 35 | 21.6 | 0.7 | 58 | 10 | AM697248 |
| c | 36 | 21.4 | 0.7 | 48 | 14 | H13556 |
| c | 37 | 21.4 | 0.7 | 50 | 9 | AU102654 |
| c | 38 | 21.4 | 0.7 | 52 | 17 | A7499115 |
| c | 39 | 21.4 | 0.7 | 53 | 14 | D18680 |
| c | 40 | 21.4 | 0.7 | 54 | 17 | A2819899 |
| c | 41 | 21.4 | 0.7 | 56 | 12 | BH247288 |
| c | 42 | 21.4 | 0.7 | 56 | 13 | BH940812 |
| c | 43 | 21.4 | 0.7 | 58 | 9 | AA514852 |
| c | 44 | 21.2 | 0.7 | 43 | 9 | AA414055 |
| c | 45 | 21.2 | 0.7 | 49 | 14 | BQ666546 |

ALIGNMENTS

| | | | | | | | |
|------------|---|--|-------|-------|---------|------------|-------------|
| RESULT 1 | H05434 | H05434 | 58 bp | mRNA | Human | EST | 11 JUN 1995 |
| LOCUS | Y180h11.s1 | Soares infant brain | 1818 | Human | sapiens | cDNA clone | |
| DEFINITION | IMAGE:4451_1 | Similar to qb:KX025 final INSULIN LIKE GROWTH FACTOR | | | | | |
| ACCESSION | H05434.1 | GI:868986 | | | | | |
| VERSION | H05434.1 | EST | | | | | |
| KEYWORDS | EST | | | | | | |
| SOURCE | human | | | | | | |
| ORGANISM | Human sapiens | | | | | | |
| REFERENCE | 1 | (bases 1 to 58) | | | | | |
| AUTHORS | Hillier, L., Clark, N., Dubuque, T., Ellington, K., Hawkins, M., Holman, M., Hultman, M., Kucab, J., Le, M., Lehoucq, G., Marra, M., Parsons, J., Rifkin, R., Rohlfing, J., Soares, M., Tate, P., Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R. | | | | | | |
| TITLE | The Washo Morek EST Project | | | | | | |
| JOURNAL | Unpublished (1995) | | | | | | |
| COMMENT | Contact: Willson RK | | | | | | |
| | Washington University School of Medicine | | | | | | |
| | 6644 Forest Park Parkway, Box 8001, St. Louis, MO 63108 | | | | | | |
| | Tel: 314 286 1800 | | | | | | |
| | Fax: 314 286 1810 | | | | | | |
| | Email: est@wustl.edu | | | | | | |
| | Insert Size: 1974 | | | | | | |
| | High quality sequence status: 1 | | | | | | |
| | High quality sequence stops: 1 | | | | | | |

[illegible]

| Query Match | 0.94 | Score 25.2 | DB 13 | Length 55 | LOCUS | A523624 | 60 bp | mRNA | linear | EST 13-APR-1999 |
|-----------------------|--------------|------------------|---------------|-----------|------------|------------|---------------|--------------|------------|---|
| Best Local Similarity | 66.7% | pred No. 1.2e+05 | | | DEFINITION | t995b12.x1 | NCI_CGAP_CLL1 | Holo sapiens | cDNA clone | MATCH:116513 |
| Matches 36 | Conservative | 0 | Mismatches 18 | Indels 0 | Gaps 0 | | | similar to | gb:X57025 | Insulin-like growth factor Ia precursor |


```

/clone="IMAGE:4950911"
/clone_lib="NCI_CGAP_Mam6"
/sex="female_virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10H"
/notes="Organ. Mammary. Vector. pCMV SpORF6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT      37 a      1 c      9 g      13 t
ORIGIN

Query Match      0.8%; Score 24; DB 13; Length 60;
Best Local Similarity 64.1%; Pred. No. 2 6e+05;
Matches 36; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2105 AATTTCGACGACACATTTCAGCAAGAAACGATATAAAGATGAAATTAATAATTC 2160
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 4 AATTTCGACGACGATATTTTTCAGCAAGAAACGATATAAAGAAACGATATAAAGG 59

RESULT 11
LOCUS      HG671284
DEFINITION      54 bp mRNA linear EST 30-APR-2003
ACCESSION      BG671284
VERSION        BG671284.1 GI:13893383
KEYWORDS      EST.
SOURCE        Norway rat.
ORGANISM      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE      1 (bases 1 to 54)
AUTHORS      Xian, H.S., Huang, Q.H., Zhang, P.X., Rao, L., Lu, Y.J., Guo, C., Yang, L.,
Huang, W.J., Fu, C., Xu, S.H., Cheng, X.P., Yan, Q., Zhu, Z.D., Zhang
X., Chen, Z., Han, Z.G. and Zhang, X.
TITLE      Identification of gene expression profile of dorsal root ganglion
in the rat peripheral axotomy model of neuropathic pain
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
MEDLINE      22056133
COMMENT      Contact: Zhang Xu
Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P R China
Tel: 86-21-64748700-121
Fax: 86-21-64713446
Email: xu.zhang@ion.ac.cn
This clone is also available at Chinese National Human Genome
Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
Pudong New Area, P.R.China. Please contact with Zhang Xu
(xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
PCR Primers
FORWARD: T3
BACKWARD: T7
Seq primer: T3
POLYA-No.

Location/Qualifiers
1..54
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="BPNR0A12"
/clone_lib="Rat DRG Library"
/sex="male"
/tissue_type="dorsal root ganglion"
/dev_stage="adult"
/notes="Total RNA was isolated from hypothalamus and
transcribed into cDNA, which was then used as template in
PCR. The PCR products were separated on sequencing gel.
The differential bands were cut, reamplified, cloned into

/clone="IMAGE:5125241"
/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10H (TI phage-resistant)"
/notes="Organ. Liver; Vector: pCMV-SpORF6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT      17 a      15 c      17 g      10 t
ORIGIN

Query Match      0.8%; Score 23.8; DB 13; Length 59;
Best Local Similarity 72.1%; Pred. No. 2 9e+05;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2687 TGAGGAACCTCGGCGCTCACAGAGGAGGCTTCACITGTTCAGCA 45
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3 TGAGGAACCTCGGCGCTCACAGAGGAGGCTTCACITGTTCAGCA 45

RESULT 13
LOCUS      B1148041
DEFINITION      602912577F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:505355 5'
ACCESSION      B1148041
VERSION        B1148041.1 GI:14508042
KEYWORDS      EST.
SOURCE        house mouse.

```


Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 2864 TCTCATTCATTTCAGTCTATTATTGAGCATCTAGTATAAGTC 2907

Db 3 TTTTTCATTCAACAAGTCTTTATTGAGGACCTACTCTCGCC 46

Search completed: April 17, 2003, 02:29:52
Job time : 4485 secs

Genome version 5.1.3
Copyright (c) 1993 2003 CompuGen Ltd.

us-09-954-679-3.rni

Search time 111 Seconds

(without alignments)

8089.636 Million cell updates/sec

Sequence: 1 aatccaaattacactcaaa.....gggaactggaatgaatt 2928

Scoring table:

IDENTITY_NOC

Gapop 10.0, Gapext 1.0

441362 seqs, 15113818 residues

Total number of hits satisfying chosen parameters: 645134

Minimum DB seq length: 0

Maximum DB seq length: 60

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

- 1: /cqn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cqn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cqn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cqn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cqn2_6/ptodata/1/ina/ptotus_COMB.seq.*
- 6: /cqn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|----|---------------------|
| 1 | 49.4 | 1.7 | 51 | 4 US-08-973-005A-4 |
| 2 | 35 | 1.2 | 35 | 4 US-08-973-005A-7 |
| 3 | 35 | 1.2 | 35 | 4 US-08-973-005A-8 |
| 4 | 25 | 0.9 | 48 | 1 US-08-783-275-6 |
| 5 | 25 | 0.9 | 48 | 1 US-08-727-708-6 |
| 6 | 23 | 0.8 | 54 | 2 US-08-418-848A-71 |
| 7 | 22.6 | 0.8 | 47 | 1 US-07-867-106-6 |
| 8 | 22.4 | 0.8 | 60 | 4 US-09-284-627-14 |
| 9 | 22.2 | 0.8 | 60 | 4 US-09-344-888A-7 |
| 10 | 21.8 | 0.7 | 39 | 4 US-09-079-984A-9 |
| 11 | 21.6 | 0.7 | 47 | 4 US-09-641-638-770 |
| 12 | 21.6 | 0.7 | 51 | 1 US-08-379-926A-2 |
| 13 | 21.6 | 0.7 | 51 | 1 US-08-379-926A-3 |
| 14 | 21 | 0.7 | 60 | 2 US-08-464-257-9 |
| 15 | 21 | 0.7 | 60 | 2 US-09-062-375-9 |
| 16 | 21 | 0.7 | 60 | 3 US-09-204-796A-9 |
| 17 | 20.8 | 0.7 | 59 | 4 US-09-542-656-12 |
| 18 | 20.8 | 0.7 | 60 | 4 US-09-188-086-12 |
| 19 | 20.6 | 0.7 | 45 | 1 US-08-483-415-21 |
| 20 | 20.6 | 0.7 | 45 | 6 5487983-18 |
| 21 | 20.6 | 0.7 | 54 | 4 US-09-171-1628-7 |
| 22 | 20.6 | 0.7 | 54 | 4 US-09-171-1628-8 |
| 23 | 20.4 | 0.7 | 57 | 4 US-09-609-816-12 |
| 24 | 20.2 | 0.7 | 46 | 4 US-09-406-074-1 |
| 25 | 20.2 | 0.7 | 47 | 4 US-09-641-638-758 |
| 26 | 20.2 | 0.7 | 51 | 4 US-09-358-972-231 |
| 27 | 20.2 | 0.7 | 51 | 4 US-09-430-615-21 |

| | | | | |
|----|------|-----|----|----------------------|
| 28 | 20.2 | 0.7 | 58 | 4 US-08-860-048-16 |
| 29 | 20.2 | 0.7 | 58 | 4 US-09-580-924-16 |
| 30 | 20.2 | 0.7 | 60 | 2 US-08-117-952-760 |
| 31 | 20 | 0.7 | 40 | 2 US-08-942-5218-4 |
| 32 | 20 | 0.7 | 49 | 3 US-09-192-792-4 |
| 33 | 20 | 0.7 | 40 | 4 US-08-445-474-4 |
| 34 | 20 | 0.7 | 40 | 5 PCT US94 02612-4 |
| 35 | 20 | 0.7 | 46 | 1 US-07-915-245-4 |
| 36 | 20 | 0.7 | 47 | 4 US-09-641-638-774 |
| 37 | 20 | 0.7 | 53 | 1 US-08-258-025A-16 |
| 38 | 20 | 0.7 | 53 | 5 PCT US95 07541-16 |
| 39 | 19.8 | 0.7 | 27 | 4 US-08-584-040-1424 |
| 40 | 19.8 | 0.7 | 45 | 2 US-08-583-276-9 |
| 41 | 19.8 | 0.7 | 46 | 2 US-08-583-276-10 |
| 42 | 19.8 | 0.7 | 47 | 4 US-09-641-638-1219 |
| 43 | 19.8 | 0.7 | 48 | 2 US-08-883-795A-14 |
| 44 | 19.8 | 0.7 | 50 | 2 US-08-054-4518-106 |
| 45 | 19.8 | 0.7 | 57 | 2 US-08-117-981-1 |

ALIGNMENTS

RESULT 1
US-08-973-005A-4
Sequence 4, Application US/08974005A
Patent No. 6320099
GENERAL INFORMATION:
APPLICANT: OGAWA, Toshiya
YOSHIOKA Masaharu
TSHIDA Tsao
TITLE OF INVENTION: VIRUS RESISTANT PLANTS EXPRESSING ANIMAL CELL DERIVED (2' 5') OLIGONUCLEOTIDE SYNTHETASE AND RIBONUCLEASE L AND A METHOD FOR CREATING THE SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Polry & Lardner
STREET: 4000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent In Release #1.0, Version #1.00
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08973-005A
FILING DATE: 01 Dec 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 134741/1995
FILING DATE: 31-MAY 1995
APPLICATION NUMBER: JP 285401/1995
FILING DATE: 01-NOV 1995
APPLICATION NUMBER: JP 52010/1996
FILING DATE: 08 MAR 1996
ATTORNEY/AGENT INFORMATION:
NAME: Reel, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKEY NUMBER: 081456/0114
TELEPHONE: (202)672-5400
TELEFAX: (202)672-5499
TELEX: 904146
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobel, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
APPLICATION NUMBER: US/08/727,708
FILING DATE: 15 JAN 1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: US/08/727,708

FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Bartfield, Neil S
REGISTRATION NUMBER: 49,901
REFERENCE/DOCKET NUMBER: 1MSC1.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619 245-8550
TELEFAX: 619 245-0176
TELEX:

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US 08 783 275 6

Query Match 0.9% Score 25; DB 1; Length 48;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 648 GGACAGGTAGAGGTCTTGAGGATTC 662

db 1 GGACAGGTAGAGGTCTTGAGGATTC 25

RESULT 5:

US 08 727 708 6

Sequence 6; Application US/08/727708

Patent No. 5,746,690

GENERAL INFORMATION:

APPLICANT: Volcani, Ariosto
APPLICANT: Mordechai, Eil
TITLE OF INVENTION: RIBONUCLEASE L INHIBITOR AS
TITLE OF INVENTION: AN INDICATOR OF CHRONIC FATIGUE SYNDROM
TITLE OF INVENTION: E
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobel, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,708

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Bartfield, Neil S
REGISTRATION NUMBER: 49,901
REFERENCE/DOCKET NUMBER: 1MSC1.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619 245-8550
TELEFAX: 619 245-0176
TELEX:

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US 08 727 708 6

Query Match

Best Local Similarity 100.0%; Score 25; DB 1; Length 48;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 638 GGACAGGTAGAGGTCTTGAGGATTC 662

db 1 GGACAGGTAGAGGTCTTGAGGATTC 25

RESULT 6:

US 08 418-848A 71/C

Sequence 71; Application US/08418848A

Patent No. 5847096

GENERAL INFORMATION:

APPLICANT: SCHUBERT, MANFRED, HARMISON II,
APPLICANT: GEORGE G., CHANG JIE, CHEN, HANJIE/EA, AKUILL
TITLE OF INVENTION: DEFECTIVE, INTERFERING
TITLE OF INVENTION: HIV PARTICLES
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 445 PARK AVENUE
CITY: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,848A

FILING DATE:

CLASSIFICATION: 526

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/946,849

FILING DATE: 28 AUG 1992

CLASSIFICATION: 526

ATTORNEY/AGENT INFORMATION:

NAME: RICHARD W. BORK

REGISTRATION NUMBER: 46,459

REFERENCE/DOCKET NUMBER: 2026 4091052

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-758 4800

TELEFAX: 212-751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 54 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-418-848A-71

Query Match

Best Local Similarity 74.4%; Score 24; DB 2; Length 54;

Mismatches 0; Indels 0; Gaps 0;

